LISTING AND AMENDMENT OF THE CLAIMS

1-25. (Canceled).

26. (Currently Amended) A method for ~~investigating a body fluid~~determining whether disseminated cancer cells are present in a blood sample from a human subject having or suspected of having cancer ~~for disseminated cancer cells, which~~, wherein the method comprises:

~~obtaining a cell-containing fraction from the body fluid with enrichment of cancer cells and determining in the cell-containing fraction the expression of at least 2 genes which are selected from the group consisting of~~

~~i) a human manganese superoxide dismutase gene;~~

~~ii) a human thioredoxin reductase 1 gene; and~~

~~iii) a human glutathione peroxidase 1 gene;~~

~~providing a further cell-containing fraction of the body fluid from the same individual and determining the expression of the genes in the further cell-containing fraction; and~~

~~comparing the expression for each of said at least 2 genes in the cell-containing fraction with its expression in the further cell-containing fraction, and~~

(a) obtaining a blood sample from a human subject having or suspected of having cancer, collecting from the blood sample a cell fraction that comprises mononuclear cells (MNC fraction), removing a fraction of the MNC fraction to obtain test fraction A', passing the remaining MNC fraction through a screen with a mesh or pore width of 17-27 μm, and collecting cells from the screen to obtain test fraction C;

(b) isolating mRNA from test fraction A' and test fraction C to obtain mRNA samples;

(c) measuring in each of the mRNA samples obtained in step (b) the expression level of manganese superoxide dismutase (MNSOD) mRNA that encodes a protein having the amino acid sequence of SEQ ID NO:13 or an allelic variant thereof, thioredoxin reductase (TXNRD1) mRNA that encodes a protein having the amino acid sequence of SEQ ID NO:15 or an allelic variant thereof, and glutathione peroxidase (GPX1) mRNA that encodes a protein having the amino acid sequence of SEQ ID NO:17 or an allelic variant thereof, wherein said measuring is by reverse transcription into cDNA and PCR;

(d) determining the expression ratio of MNSOD, TXNRD1, and GPX1 from test fraction C to test fraction A'; and

(e) comparing the expression ratio for each of MNSOD, TXNRD1, and GPX1 determined in step (d) to a control limit for expression for each of MNSOD, TXNRD1, and GPX1 in blood samples of healthy human subjects,

and wherein ~~the body fluid is selected from blood and bone marrow and an elevated expression of at least one of said at least 2 genes determined in the cell-containing fraction, as compared to its expression in the further cell-containing fraction,~~ an expression ratio determined in step (d) higher than the control limit of expression of at least one of MNSOD, TXNRD1 andGPX1 indicates the presence of disseminated cancer cells in the ~~body fluid~~ blood sample from a human subject having or suspected of having cancer.

27-31. (Canceled).

32. (Currently Amended) The method ~~as claimed in~~of claim 26, wherein the ~~elevated expression of at least one of said genes~~presence of disseminated cancer cells in the blood sample from a human subject having or suspected of having cancer indicates the presence of a tumor.

33. (Canceled).

34. (Currently Amended) The method ~~as claimed in~~of claim 26, wherein the ~~elevated expression of at least one of said genes~~presence of disseminated cancer cells in the blood sample from a human subject having or suspected of having cancer indicates a risk to develop a metastasis or a recurrence.

35-45. (Canceled).

46. (Currently Amended) The method ~~as claimed in~~of claim ~~29~~26, wherein the screen has a mesh or pore width of about 20 μm.

47-70. (Canceled).

71. (New) The method of claim 26, wherein the cDNA obtained by reverse transcription comprises the nucleotide sequences of SEQ ID NO:1 and 2 for MNSOD mRNA; SEQ ID NO:4 and 5 for TXNRD1 mRNA, and SEQ ID NO:7 and 8 for GPX1 mRNA.

72. (New) The method of claim 71, wherein the control limit for expression has been determined by performing the following steps:

(f) obtaining blood samples from healthy human subjects not suffering from cancer, collecting a cell fraction that comprises mononuclear cells (MNC fraction) from the blood samples, removing a fraction of the MNC fraction to obtain reference fraction A', passing the remaining MNC fraction through a screen with a mesh or pore width of 17-27 μm mesh, and collecting cells from the screen to obtain reference fraction C;

(g) optionally isolating CD45-positive lymphocytes from reference fraction A' to obtain reference fraction A,

(h) isolating mRNA from reference fraction A' or A and reference fraction C to obtain mRNA samples;

(i) measuring in each of the mRNA samples obtained in step (h) the expression level of MNSOD mRNA that encodes a protein having the amino acid sequence of SEQ ID NO:13 or an allelic variant thereof, TXNRD1 mRNA that encodes a protein having the amino acid sequence of SEQ ID NO:15 or an allelic variant thereof, and GPX1 mRNA that encodes a protein having the amino acid sequence of SEQ ID NO:17 or an allelic variant thereof, wherein said measuring is by reverse transcription into cDNA and PCR; and

(j) determining the average for the expression ratio of MNSOD, TXNRD1, and GPX1 from reference fraction C to reference fraction A' or A, and determining a control limit for expression.

73. (New) The method of claim 71, wherein the control limit for expression has been determined by performing the following steps:

(f) obtaining blood samples from healthy human subjects not suffering from cancer, collecting a cell fraction that comprises mononuclear cells (MNC fraction) from the blood samples, removing a fraction of the MNC fraction to obtain reference fraction A', passing the remaining MNC fraction through a screen with a mesh or pore width of 17-27 μm mesh, and collecting cells from the screen to obtain reference fraction C;

(g) isolating CD45-positive lymphocytes from reference fraction A' to obtain reference fraction A,

(h) isolating mRNA from reference fraction A and reference fraction C to obtain mRNA samples;

(i) measuring in each of the mRNA samples obtained in step (h) the expression level of MNSOD mRNA that encodes a protein having the amino acid sequence of SEQ ID NO:13 or an allelic variant thereof, TXNRD1 mRNA that encodes a protein having the amino acid sequence of SEQ ID NO:15 or an allelic variant thereof, and GPX1 mRNA that encodes a protein having the amino acid sequence of SEQ ID NO:17 or an allelic variant thereof, wherein said measuring is by reverse transcription into cDNA and PCR; and

(j) determining the average and standard deviation for the expression ratio of MNSOD, TXNRD1, and GPX1 from reference fraction C to reference fraction A, and determining a control limit for expression.